

Figure 1

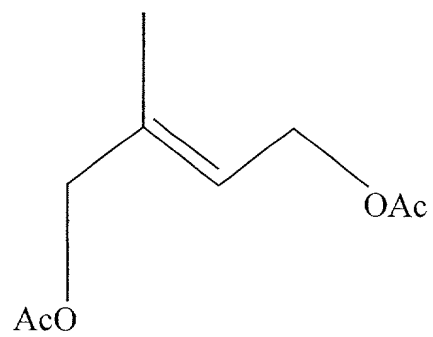


FIGURE 2

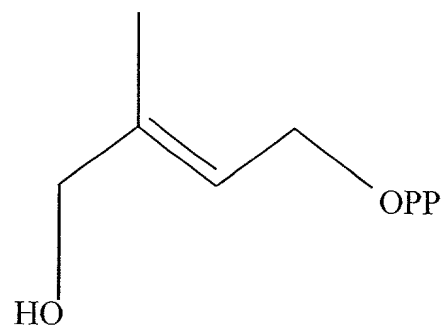


FIGURE 3

EcgcpE	:MHNQAPIORRKSTRIYVGNVPICDG	: 25
AtgcpE	:	MATGVLPAVSGIKIPDSKVGFKSMNLVRICDVRSLRSARRRVSVIENSQSDLAELQPASEGSPLLVPRQKYCESLHKTTRRKRTRIVMVGNVALGSE	: 100
EcgcpE	:	APIAVQSMTNVRTDVETVNQKALERVGADIVRVSPTMDAAEAF.....KLTKQOVNPLVADIHFDIRALKVAEYGVDQRPNPGNIEN.....	: 114
AtgcpE	:	HPIRCQWITSDTKDTCTVDEVMRLADKGADIVRVCKKEADACFEIKDKILOINYNPLVADIHFAPTALFVAEC.FDLRNPNGNFADRAAQFE	: 199
EcgcpE	:EERIRMVJCCARDKNIPIRIGVNWAGSLEKDIOEKYGPPEFOALLIESAMRHVDHLDRLENDDOFKVSVKASDVFIJAVESRYLLAKQ	: 198
AtgcpE	:	TIDYTEDEYQKELQHIEQVFTPLVEKKYKGRAMRGINHGISLSDEIMSYGDPSPROMYESAFFEFARI CRKLDXHNFFVFSMKASNPIVMVQAURLVAE	: 298
EcgcpE	:	I....DOPLHLGTEAGCARSGAVKSAIGGLLSGGTGTURVSLAADPVEELK.....	: 249
AtgcpE	:	MYVHGWDYPLHLGVTEAGEGEDGRMKSAIGLTILLOGLGDTIRVSLITEPPEEEEDPCRRLANLGTKAAKLOQGAPPFEKHRHYFDQRRRTGDLPVQKEG	: 398
EcgcpE	:EEVDYRNVLRHDGSVLMSISLDQLKAPELLYRSLATKLWVGMPFKDLATVDSILLRELPPVDDQVARLAKRLIDVSMGVIAPLSELTKPLPNAMVLVN	: 498
AtgcpE	:LKELSGGAYKLLPEGTRLVWSLRGDEPYEELEILKNIDATMILHDVPFTEDKVSrvHAARRLFELSSENSVNPFIHHINFPTGIHRDELVIHAGTYAGG	: 598
EcgcpE	:VGEFDILKSIRSRGINFLACBTCRSRQEFDVIGTVNALEQBLEDAITPMDASHIGCVNGPGGEALVSTIGVTGNNK	: 325
AtgcpE	:	LLVDGLGDGMLEAPDQDFDLRNTSENLLQGCVRMNTKTEYVSCBSCGRITLFDLQEI SAEIREKTSHLPG.VSLAIMGCHVNGPGEMADADFVYGGSP	: 697
EcgcpE	:	.KSGLYBEDG.VKRKRdNDNMIDOEARIIRAKASOLDEARRFDVQQVHK	: 372
AtgcpE	:	GKIDLTVGKTWVRGTAATEATDALIGLIKHEG.....RWVDDPPVADE	: 740

Figure 4

pZL1 (135H1):

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...[SalI]aaaaatcg(...)gaaaaATGGCGACTGGAGTATTGCCAGCTCCGGTTTCTGGGATCAAG
      M A T G V L P A P V S G I K
ATACCGGATTTCGAAAGTCGGGTTTGGTAAAGCATGAATCTTGTGAGAAATTTGTGATGTTAGGAGTCTA
I P D S K V G F G K S M N L V R I C D V R S L
BglII
AGATCTGCT(...)GATGAGTAGatttc(...)ataaaagt[NotI]/[XbaI]/[BamHI]/[HindIII]/[SphI]...
R S A (...) D E *
      ↑

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pQE30:

```

      BamHI
      ▼
      SphI

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pQE-AGH:

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      BamHI/BglII
      ▼
      SphI
      GATCTGCT(...)GATGAGTAGatttc(...)...
      S A (...) D E *

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Figure 5